

SEQUENCE LISTING

<110> VAISVILA, ROMUALDAS
MORGAN, RICHARD D.
KUCERA, REBECCA B.
CLAUS, TOBY E.
RALEIGH, ELISABETH A.



<120> METHOD FOR CLONING AND PRODUCING THE MseI RESTRICTION
ENDONUCLEASE

<130> NEB-181

<140> 09/689,343

<141> 2000-10-12

<160> 9

<170> PatentIn Ver. 2.0

<210> 1

<211> 903

<212> DNA

<213> Micrococcus sp.

<220>

<221> CDS

<222> (1)..(900)

<400> 1

atg cct atc tcg acc gtc tgg acg ccg gac gga gac gac ctc atc gtg	48
Met Pro Ile Ser Thr Val Trp Thr Pro Asp Gly Asp Asp Leu Ile Val	
1 5 10 15	
gag gcg gac aac ctc gat ttc att caa acg ctc ccc gac gcg agc ttc	96
Glu Ala Asp Asn Leu Asp Phe Ile Gln Thr Leu Pro Asp Ala Ser Phe	
20 25 30	
cga atg atc tac atc gat ccg ccg ttc aac aca ggg cga acg cag cgg	144
Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg	
35 40 45	
ctt cag tcg ctc aag acg acc cgc tcg gtc aca ggg tcg cga gtc ggc	192
Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly	
50 55 60	
ttc aaa ggc cag acg tac gac acg gtc aag agc act ctg cac tcg tat	240
Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr	
65 70 75 80	
gac gac gct ttc acc gac tat tgg tcg ttc ctc gaa ccg cgt ctc ctg	288
Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu	
85 90 95	
gag gct tgg cgg tgg ctc acc cct gac ggc gcg ctc tat ctt cat ctg	336
Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu	
100 105 110	
gat tac cgc gag gtt cac tac gcc aag gtc gtc ctc gac gcg atg ttc	384
Asp Tyr Arg Glu Val His Tyr Ala Lys Val Val Leu Asp Ala Met Phe	
115 120 125	

RECEIVED
APR 05 2002
TECH CENTER 1600/2900

gga cgc gaa agc ttc ctg aac gag ctg atc tgg gcg tac gac tac ggc 432
 Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly
 130 135 140

gcg cgc tcg aag agc aag tgg ccc acc aag cac gac aac atc ctc gtg 480
 Ala Arg Ser Lys Ser Lys Trp Pro Thr Lys His Asp Asn Ile Leu Val
 145 150 155 160

tat gtg aag gac ccg aac aac tac gtc tgg aac ggt cag gat gta gat 528
 Tyr Val Lys Asp Pro Asn Asn Tyr Val Trp Asn Gly Gln Asp Val Asp
 165 170 175

gcg gag ccc tac atg gcg ccc ggg ctc gtt aca ccc gag aag gta gcg 576
 Arg Glu Pro Tyr Met Ala Pro Gly Leu Val Thr Pro Glu Lys Val Ala
 180 185 190

ctt ggc aag ctg ccc acc gac gtc tgg tgg cac aca atc gtt ccg cct 624
 Leu Gly Lys Leu Pro Thr Asp Val Trp Trp His Thr Ile Val Pro Pro
 195 200 205

gcg agc aaa gag cgc acc ggg tac gcg aca cag aag ccg gtc ggc atc 672
 Ala Ser Lys Glu Arg Thr Gly Tyr Ala Thr Gln Lys Pro Val Gly Ile
 210 215 220

atc cgt cgc atg att cag gcg agc agc aat gaa ggc gac tgg gtt ctg 720
 Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu
 225 230 235 240

gat ttc ttc gct ggt agt ggg acg acc ggc gcc gcg gcc cgc cag ctc 768
 Asp Phe Phe Ala Gly Ser Gly Thr Thr Gly Ala Ala Ala Arg Gln Leu
 245 250 255

gga cgc cgt ttt gtg ctc gta gac gtc aac cca gaa gca atc gcg gta 816
 Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val
 260 265 270

atg gca aaa cgg ttg gat gac ggg gca ttg gac acc agc gtg acg atc 864
 Met Ala Lys Arg Leu Asp Asp Gly Ala Leu Asp Thr Ser Val Thr Ile
 275 280 285

gtg cag act ccc cag agt gac cca cga acc gac gga tga 903
 Val Gln Thr Pro Gln Ser Asp Pro Arg Thr Asp Gly
 290 295 300

<210> 2

<211> 300

<212> PRT

<213> Micrococcus sp.

<400> 2

Met Pro Ile Ser Thr Val Trp Thr Pro Asp Gly Asp Asp Leu Ile Val
 1 5 10 15

Glu Ala Asp Asn Leu Asp Phe Ile Gln Thr Leu Pro Asp Ala Ser Phe
 20 25 30

Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg
 35 40 45

Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly
 50 55 60

Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr
65 70 75 80
Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu
85 90 95
Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu
100 105 110
Asp Tyr Arg Glu Val His Tyr Ala Lys Val Val Leu Asp Ala Met Phe
115 120 125
Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly
130 135 140
Ala Arg Ser Lys Ser Lys Trp Pro Thr Lys His Asp Asn Ile Leu Val
145 150 155 160
Tyr Val Lys Asp Pro Asn Asn Tyr Val Trp Asn Gly Gln Asp Val Asp
165 170 175
Arg Glu Pro Tyr Met Ala Pro Gly Leu Val Thr Pro Glu Lys Val Ala
180 185 190
Leu Gly Lys Leu Pro Thr Asp Val Trp Trp His Thr Ile Val Pro Pro
195 200 205
Ala Ser Lys Glu Arg Thr Gly Tyr Ala Thr Gln Lys Pro Val Gly Ile
210 215 220
Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu
225 230 235 240
Asp Phe Phe Ala Gly Ser Gly Thr Thr Gly Ala Ala Ala Arg Gln Leu
245 250 255
Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val
260 265 270
Met Ala Lys Arg Leu Asp Asp Gly Ala Leu Asp Thr Ser Val Thr Ile
275 280 285
Val Gln Thr Pro Gln Ser Asp Pro Arg Thr Asp Gly
290 295 300

<210> 3

<211> 1236

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism: ENVIRONMENTAL DNA

<220>

<221> CDS

<222> (1) .. (1233)

<220>

<223> At position 594, N = G, A, C or T

<400> 3

atg cct aca ctg gat tgg ccc ggt aaa cag tta agc ttc cca cca gct	48
Met Pro Thr Leu Asp Trp Pro Gly Lys Gln Leu Ser Phe Pro Pro Ala	
1 5 10 15	
acc tcc ttg cat ctg gag agt gtg gtc act gag gga gcg gag tca ccg	96
Thr Ser Leu His Leu Glu Ser Val Val Thr Glu Gly Ala Glu Ser Pro	
20 25 30	
cct aat cgt ctg att tgg gcg gac aac ctg ccg cta atg gta gat ttg	144
Pro Asn Arg Leu Ile Trp Ala Asp Asn Leu Pro Leu Met Val Asp Leu	
35 40 45	
ttg gcc gaa tat gaa ggg aaa atc gat ctg atc tac gcc gat ccc cct	192
Leu Ala Glu Tyr Glu Gly Lys Ile Asp Leu Ile Tyr Ala Asp Pro Pro	
50 55 60	
ttt ttt acg gat cgt act tat gcg gcg cga att ggt cat ggg gag gat	240
Phe Phe Thr Asp Arg Thr Tyr Ala Ala Arg Ile Gly His Gly Glu Asp	
65 70 75 80	
tcg cgt cgt cca caa acc tgg cag ctt gca gaa gga tat acg gac gag	288
Ser Arg Arg Pro Gln Thr Trp Gln Leu Ala Glu Gly Tyr Thr Asp Glu	
85 90 95	
tgg aag gat tta gat gaa tac ctg gac ttc ctt tat cca cgc ctg gta	336
Trp Lys Asp Leu Asp Glu Tyr Leu Asp Phe Leu Tyr Pro Arg Leu Val	
100 105 110	
ctg atg tat cga ctg ctg gca cca cac gga acg ctc tac ttg cac ctg	384
Leu Met Tyr Arg Leu Leu Ala Pro His Gly Thr Leu Tyr Leu His Leu	
115 120 125	
gac tgg cac gcc aat gcc tac gta cgt gta ctg ctt gat gag atc ttc	432
Asp Trp His Ala Asn Ala Tyr Val Arg Val Leu Leu Asp Glu Ile Phe	
130 135 140	
ggg cga cag cgg ttt ctc aac gag atc gtc tgg atc tat cac ggc ccc	480
Gly Arg Gln Arg Phe Leu Asn Glu Ile Val Trp Ile Tyr His Gly Pro	
145 150 155 160	
tca gcc atc cga cgc gcc ttc aag cgc aaa cat gat acc atc ttg gtt	528
Ser Ala Ile Arg Arg Ala Phe Lys Arg Lys His Asp Thr Ile Leu Val	
165 170 175	
tat gtg aaa ggt gaa aac tat aca ttc aat gcg gat gcg gtt cgt caa	576
Tyr Val Lys Gly Glu Asn Tyr Thr Phe Asn Ala Asp Ala Val Arg Gln	
180 185 190	
cct tac cat ccg agc acn cat aag acc ttc gct tcc tcc ccg aag gcc	624
Pro Tyr His Pro Ser Xaa His Lys Thr Phe Ala Ser Ser Pro Lys Ala	
195 200 205	
ggc ttt ggt aag gtg ccg gat ctg cag cgc ggc aaa gtg ccc gaa gac	672
Gly Phe Gly Lys Val Pro Asp Leu Gln Arg Gly Lys Val Pro Glu Asp	
210 215 220	
tgg tgg tat ttt ccg gtc gtg gcc cgt cta cac cga gaa cgg agc ggc	720
Trp Trp Tyr Phe Pro Val Val Ala Arg Leu His Arg Glu Arg Ser Gly	
225 230 235 240	

tat	ccg	act	caa	aag	cct	caa	gcc	ttg	ctg	gag	cgg	atc	ctg	ctg	gcc	768
Tyr	Pro	Thr	Gln	Lys	Pro	Gln	Ala	Leu	Leu	Glu	Arg	Ile	Leu	Leu	Ala	
			245					250							255	
tcc	tcg	aac	gca	ggc	gat	ctg	gtg	gca	gac	ttc	ttc	tgc	ggc	tca	ggg	816
Ser	Ser	Asn	Ala	Gly	Asp	Leu	Val	Ala	Asp	Phe	Phe	Cys	Gly	Ser	Gly	
			260					265					270			
aca	acc	gct	gtg	gtg	gca	gcc	cgt	ctg	gga	cgg	cgc	ttc	ctg	gtc	aac	864
Thr	Thr	Ala	Val	Val	Ala	Ala	Arg	Leu	Gly	Arg	Arg	Phe	Leu	Val	Asn	
			275				280					285				
gat	gca	agc	tgg	cgc	gcc	gtt	cat	gtg	aca	cgc	aca	cgc	ttg	cta	cgc	912
Asp	Ala	Ser	Trp	Arg	Ala	Val	His	Val	Thr	Arg	Thr	Arg	Leu	Leu	Arg	
			290			295					300					
gag	gga	gta	agt	ttc	act	ttt	gaa	cgc	cag	gaa	act	ttt	act	cta	cct	960
Glu	Gly	Val	Ser	Phe	Thr	Phe	Glu	Arg	Gln	Glu	Thr	Phe	Thr	Leu	Pro	
			305			310				315					320	
atc	cag	cca	ctt	cca	cca	gat	tgg	ttg	atc	atc	gcc	gag	gag	cag	att	1008
Ile	Gln	Pro	Leu	Pro	Pro	Asp	Trp	Leu	Ile	Ile	Ala	Glu	Glu	Gln	Ile	
			325					330						335		
cgc	ctc	caa	gca	ccc	ttt	ctc	gta	gat	ttt	tgg	gaa	gtg	gac	gat	caa	1056
Arg	Leu	Gln	Ala	Pro	Phe	Leu	Val	Asp	Phe	Trp	Glu	Val	Asp	Asp	Gln	
			340					345					350			
tgg	gat	ggc	aaa	atc	ttc	cgc	agc	cgt	cat	caa	ggc	tta	cgc	tcc	cgc	1104
Trp	Asp	Gly	Lys	Ile	Phe	Arg	Ser	Arg	His	Gln	Gly	Leu	Arg	Ser	Arg	
			355				360					365				
ctt	cag	gag	cag	gcg	ccg	ctc	tct	cta	cca	ttg	acc	ggg	aat	gga	ctg	1152
Leu	Gln	Glu	Gln	Ala	Pro	Leu	Ser	Leu	Pro	Leu	Thr	Gly	Asn	Gly	Leu	
			370			375					380					
ttg	tgt	gta	cgg	gta	gtg	agc	cgt	gaa	ggg	gaa	tac	tat	gag	ttc	aca	1200
Leu	Cys	Val	Arg	Val	Val	Ser	Arg	Glu	Gly	Glu	Tyr	Tyr	Glu	Phe	Thr	
			385			390			395						400	
ggt	cga	gcc	gat	agc	cct	cac	ccc	gta	tcg	ttt	tga					1236
Gly	Arg	Ala	Asp	Ser	Pro	His	Pro	Val	Ser	Phe						
				405				410								

<210> 4

<211> 411

<212> PRT

<213> Unknown

<220>

<223> At position 198, Xaa = any amino acid

<400> 4

Met	Pro	Thr	Leu	Asp	Trp	Pro	Gly	Lys	Gln	Leu	Ser	Phe	Pro	Pro	Ala
1				5					10					15	

Thr	Ser	Leu	His	Leu	Glu	Ser	Val	Val	Thr	Glu	Gly	Ala	Glu	Ser	Pro
			20					25					30		

Pro	Asn	Arg	Leu	Ile	Trp	Ala	Asp	Asn	Leu	Pro	Leu	Met	Val	Asp	Leu
			35				40					45			

Leu	Ala	Glu	Tyr	Glu	Gly	Lys	Ile	Asp	Leu	Ile	Tyr	Ala	Asp	Pro	Pro	50	55	60
Phe	Phe	Thr	Asp	Arg	Thr	Tyr	Ala	Ala	Arg	Ile	Gly	His	Gly	Glu	Asp	65	70	75
Ser	Arg	Arg	Pro	Gln	Thr	Trp	Gln	Leu	Ala	Glu	Gly	Tyr	Thr	Asp	Glu	85	90	95
Trp	Lys	Asp	Leu	Asp	Glu	Tyr	Leu	Asp	Phe	Leu	Tyr	Pro	Arg	Leu	Val	100	105	110
Leu	Met	Tyr	Arg	Leu	Leu	Ala	Pro	His	Gly	Thr	Leu	Tyr	Leu	His	Leu	115	120	125
Asp	Trp	His	Ala	Asn	Ala	Tyr	Val	Arg	Val	Leu	Leu	Asp	Glu	Ile	Phe	130	135	140
Gly	Arg	Gln	Arg	Phe	Leu	Asn	Glu	Ile	Val	Trp	Ile	Tyr	His	Gly	Pro	145	150	155
Ser	Ala	Ile	Arg	Arg	Ala	Phe	Lys	Arg	Lys	His	Asp	Thr	Ile	Leu	Val	165	170	175
Tyr	Val	Lys	Gly	Glu	Asn	Tyr	Thr	Phe	Asn	Ala	Asp	Ala	Val	Arg	Gln	180	185	190
Pro	Tyr	His	Pro	Ser	Xaa	His	Lys	Thr	Phe	Ala	Ser	Ser	Pro	Lys	Ala	195	200	205
Gly	Phe	Gly	Lys	Val	Pro	Asp	Leu	Gln	Arg	Gly	Lys	Val	Pro	Glu	Asp	210	215	220
Trp	Trp	Tyr	Phe	Pro	Val	Val	Ala	Arg	Leu	His	Arg	Glu	Arg	Ser	Gly	225	230	235
Tyr	Pro	Thr	Gln	Lys	Pro	Gln	Ala	Leu	Leu	Glu	Arg	Ile	Leu	Leu	Ala	245	250	255
Ser	Ser	Asn	Ala	Gly	Asp	Leu	Val	Ala	Asp	Phe	Phe	Cys	Gly	Ser	Gly	260	265	270
Thr	Thr	Ala	Val	Val	Ala	Ala	Arg	Leu	Gly	Arg	Arg	Phe	Leu	Val	Asn	275	280	285
Asp	Ala	Ser	Trp	Arg	Ala	Val	His	Val	Thr	Arg	Thr	Arg	Leu	Leu	Arg	290	295	300
Glu	Gly	Val	Ser	Phe	Thr	Phe	Glu	Arg	Gln	Glu	Thr	Phe	Thr	Leu	Pro	305	310	315
Ile	Gln	Pro	Leu	Pro	Pro	Asp	Trp	Leu	Ile	Ile	Ala	Glu	Glu	Gln	Ile	325	330	335
Arg	Leu	Gln	Ala	Pro	Phe	Leu	Val	Asp	Phe	Trp	Glu	Val	Asp	Asp	Gln	340	345	350
Trp	Asp	Gly	Lys	Ile	Phe	Arg	Ser	Arg	His	Gln	Gly	Leu	Arg	Ser	Arg	355	360	365

```

Leu Gln Glu Gln Ala Pro Leu Ser Leu Pro Leu Thr Gly Asn Gly Leu
370                               375                               380

Leu Cys Val Arg Val Val Ser Arg Glu Gly Glu Tyr Tyr Glu Phe Thr
385                               390                               395                               400

Gly Arg Ala Asp Ser Pro His Pro Val Ser Phe
                               405                               410

```

<210> 5

<211> 924

<212> DNA

<213> Unknown

<220>

<223> Description of Unknown Organism: ENVIRONMENTAL DNA

<220>

<221> CDS

<222> (1)..(921)

<400> 5

```

atg atc acg aac ctg atg gaa aac gat gtc att ggc aaa atc tac ttt      48
Met Ile Thr Asn Leu Met Glu Asn Asp Val Ile Gly Lys Ile Tyr Phe
  1                               5                               10                               15

gcc gac aac atg gaa gtc ctg cga ggg ctt ccg gcg gcg tcc gtg gac      96
Ala Asp Asn Met Glu Val Leu Arg Gly Leu Pro Ala Ala Ser Val Asp
                20                               25                               30

ctg atc tac atc gat cct ccg ttc aac acc gga aag gtt cag gag cgc      144
Leu Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Lys Val Gln Glu Arg
                35                               40                               45

act cag ctc aaa acg gtg cgc tcc gag tgg ggc gat cgc gtc gga ttc      192
Thr Gln Leu Lys Thr Val Arg Ser Glu Trp Gly Asp Arg Val Gly Phe
                50                               55                               60

cag ggc cgt cgc tac gaa agc atc gtc gtg ggt aag aag cgc ttt acc      240
Gln Gly Arg Arg Tyr Glu Ser Ile Val Val Gly Lys Lys Arg Phe Thr
                65                               70                               75                               80

gac ttc ttc gac gac tat ctg gct ttc ctg gaa ccg cgc ctg gtc gaa      288
Asp Phe Phe Asp Asp Tyr Leu Ala Phe Leu Glu Pro Arg Leu Val Glu
                85                               90                               95

gcc cat cgt gtt ctg gcg ccg cac ggg tgc ctc tac ttt cac gtc gac      336
Ala His Arg Val Leu Ala Pro His Gly Cys Leu Tyr Phe His Val Asp
                100                               105                               110

tac cgc gag gtg cac tac tgt aag gtc ctt ctt gac ggc atc ttc ggt      384
Tyr Arg Glu Val His Tyr Cys Lys Val Leu Leu Asp Gly Ile Phe Gly
                115                               120                               125

cgc gag gcc ttt ctc aac gag atc atc tgg gcc tac gat tac ggc ggg      432
Arg Glu Ala Phe Leu Asn Glu Ile Ile Trp Ala Tyr Asp Tyr Gly Gly
                130                               135                               140

cgt ccg aag gac agg tgg cct cct aag cac gac aac atc ctg ctc tac      480
Arg Pro Lys Asp Arg Trp Pro Pro Lys His Asp Asn Ile Leu Leu Tyr
                145                               150                               155                               160

```

gcc aag act ccc ggt cgc cac gtg ttc aat gcg gac gaa atc gag cgc 528
 Ala Lys Thr Pro Gly Arg His Val Phe Asn Ala Asp Glu Ile Glu Arg
 165 170 175

att ccc tac atg gct ccg ggc ctg gtt ggc ccc gaa aag gca gcc cgt 576
 Ile Pro Tyr Met Ala Pro Gly Leu Val Gly Pro Glu Lys Ala Ala Arg
 180 185 190

gga aaa ctg cca acc gac acg tgg tgg cat acg atc gtt ccg acc agc 624
 Gly Lys Leu Pro Thr Asp Thr Trp Trp His Thr Ile Val Pro Thr Ser
 195 200 205

ggc tcc gag aag acc ggg tat cca acc cag aaa cct tta ggg att ctc 672
 Gly Ser Glu Lys Thr Gly Tyr Pro Thr Gln Lys Pro Leu Gly Ile Leu
 210 215 220

cgc cgt att gtg cag gca tcg tct cat ccg ggg gca gtc gtg ctc gac 720
 Arg Arg Ile Val Gln Ala Ser Ser His Pro Gly Ala Val Val Leu Asp
 225 230 235 240

ttc ttc gcc ggc agt ggg aca aca ggg gta gcg gct ttt gag ttg ggc 768
 Phe Phe Ala Gly Ser Gly Thr Thr Gly Val Ala Ala Phe Glu Leu Gly
 245 250 255

cgg cgt ttc att ctg gtc gat aac cat ccg gag gcc ctc cag gtg atg 816
 Arg Arg Phe Ile Leu Val Asp Asn His Pro Glu Ala Leu Gln Val Met
 260 265 270

gcc agg cgc ttc gac ggc atc gag ggg atc gaa tgg gtg ggc ttc gat 864
 Ala Arg Arg Phe Asp Gly Ile Glu Gly Ile Glu Trp Val Gly Phe Asp
 275 280 285

ccg aca ccg tac cag aag ggc gca aag cag cgc cgc tcc tgc ccg gcg 912
 Pro Thr Pro Tyr Gln Lys Gly Ala Lys Gln Arg Arg Ser Cys Pro Ala
 290 295 300

ccc acc ggg taa 924
 Pro Thr Gly
 305

<210> 6
 <211> 307
 <212> PRT
 <213> Unknown

<400> 6
 Met Ile Thr Asn Leu Met Glu Asn Asp Val Ile Gly Lys Ile Tyr Phe
 1 5 10 15
 Ala Asp Asn Met Glu Val Leu Arg Gly Leu Pro Ala Ala Ser Val Asp
 20 25 30
 Leu Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Lys Val Gln Glu Arg
 35 40 45
 Thr Gln Leu Lys Thr Val Arg Ser Glu Trp Gly Asp Arg Val Gly Phe
 50 55 60
 Gln Gly Arg Arg Tyr Glu Ser Ile Val Val Gly Lys Lys Arg Phe Thr
 65 70 75 80

Asp Phe Phe Asp Asp Tyr Leu Ala Phe Leu Glu Pro Arg Leu Val Glu
 85 90 95
 Ala His Arg Val Leu Ala Pro His Gly Cys Leu Tyr Phe His Val Asp
 100 105 110
 Tyr Arg Glu Val His Tyr Cys Lys Val Leu Leu Asp Gly Ile Phe Gly
 115 120 125
 Arg Glu Ala Phe Leu Asn Glu Ile Ile Trp Ala Tyr Asp Tyr Gly Gly
 130 135 140
 Arg Pro Lys Asp Arg Trp Pro Pro Lys His Asp Asn Ile Leu Leu Tyr
 145 150 155 160
 Ala Lys Thr Pro Gly Arg His Val Phe Asn Ala Asp Glu Ile Glu Arg
 165 170 175
 Ile Pro Tyr Met Ala Pro Gly Leu Val Gly Pro Glu Lys Ala Ala Arg
 180 185 190
 Gly Lys Leu Pro Thr Asp Thr Trp Trp His Thr Ile Val Pro Thr Ser
 195 200 205
 Gly Ser Glu Lys Thr Gly Tyr Pro Thr Gln Lys Pro Leu Gly Ile Leu
 210 215 220
 Arg Arg Ile Val Gln Ala Ser Ser His Pro Gly Ala Val Val Leu Asp
 225 230 235 240
 Phe Phe Ala Gly Ser Gly Thr Thr Gly Val Ala Ala Phe Glu Leu Gly
 245 250 255
 Arg Arg Phe Ile Leu Val Asp Asn His Pro Glu Ala Leu Gln Val Met
 260 265 270
 Ala Arg Arg Phe Asp Gly Ile Glu Gly Ile Glu Trp Val Gly Phe Asp
 275 280 285
 Pro Thr Pro Tyr Gln Lys Gly Ala Lys Gln Arg Arg Ser Cys Pro Ala
 290 295 300
 Pro Thr Gly
 305

<210> 7
 <211> 561
 <212> DNA
 <213> Micrococcus sp.

<220>
 <221> CDS
 <222> (1)..(558)

<400> 7
 gtg acc cac gaa ccg acg gat gat ccc gat ttc ata gtg atg gcc gcg 48
 Val Thr His Glu Pro Thr Asp Asp Pro Asp Phe Ile Val Met Ala Ala
 1 5 10 15

agc gcg gcg aac ctc gct gat cgg tac gta gcg agt gaa gac gac ccc 96
 Ser Ala Ala Asn Leu Ala Asp Arg Tyr Val Ala Ser Glu Asp Asp Pro
 20 25 30

tgg gtc ggc agc ccg ttc gag tgg atc ctt cgc gtt cca tcc aga acg 144
 Trp Val Gly Ser Pro Phe Glu Trp Ile Leu Arg Val Pro Ser Arg Thr
 35 40 45

aag ggc gcg gtc ggt gag ctg ctc gtg agc gaa tgg gct aat gcc aaa 192
 Lys Gly Ala Val Gly Glu Leu Leu Val Ser Glu Trp Ala Asn Ala Lys
 50 55 60

ggc ctc cgt gtg aag agg tcg ggg tcc agc gat gcg gac cgc gtg atc 240
 Gly Leu Arg Val Lys Arg Ser Gly Ser Ser Asp Ala Asp Arg Val Ile
 65 70 75 80

aac ggg cat cgc atc gag atc aag atg tcg act ttg tgg aag tcc ggc 288
 Asn Gly His Arg Ile Glu Ile Lys Met Ser Thr Leu Trp Lys Ser Gly
 85 90 95

ggc ttc aag ttt cag cag atc cgg gat cag gag tac gac ttt tgc ctc 336
 Gly Phe Lys Phe Gln Gln Ile Arg Asp Gln Glu Tyr Asp Phe Cys Leu
 100 105 110

tgc ctt ggg atc agc ccg ttc gaa gtg cac gcg tgg ctg ctg ccc aaa 384
 Cys Leu Gly Ile Ser Pro Phe Glu Val His Ala Trp Leu Leu Pro Lys
 115 120 125

gac cta ttg ctt gag tac gtg att ggt cac atg ggt cag cac acc ggc 432
 Asp Leu Leu Leu Glu Tyr Val Ile Gly His Met Gly Gln His Thr Gly
 130 135 140

gcg agc ggg agc gac act gcg tgg ctg ggg ttc cca gcg gac gag ccg 480
 Ala Ser Gly Ser Asp Thr Ala Trp Leu Gly Phe Pro Ala Asp Glu Pro
 145 150 155 160

tat gac tgg atg cgc cct ttc gga ggt cgc tta ggt cac gtc gaa gat 528
 Tyr Asp Trp Met Arg Pro Phe Gly Gly Arg Leu Gly His Val Glu Asp
 165 170 175

ctc ctc ctc gcg gcc ggc ccc ggt ccc tac tga 561
 Leu Leu Leu Ala Ala Gly Pro Gly Pro Tyr
 180 185

<210> 8
 <211> 186
 <212> PRT
 <213> Micrococcus sp.

<400> 8
 Val Thr His Glu Pro Thr Asp Asp Pro Asp Phe Ile Val Met Ala Ala
 1 5 10 15

Ser Ala Ala Asn Leu Ala Asp Arg Tyr Val Ala Ser Glu Asp Asp Pro
 20 25 30

Trp Val Gly Ser Pro Phe Glu Trp Ile Leu Arg Val Pro Ser Arg Thr
 35 40 45

Lys Gly Ala Val Gly Glu Leu Leu Val Ser Glu Trp Ala Asn Ala Lys
 50 55 60

Gly Leu Arg Val Lys Arg Ser Gly Ser Ser Asp Ala Asp Arg Val Ile
 65 70 75 80
 Asn Gly His Arg Ile Glu Ile Lys Met Ser Thr Leu Trp Lys Ser Gly
 85 90 95
 Gly Phe Lys Phe Gln Gln Ile Arg Asp Gln Glu Tyr Asp Phe Cys Leu
 100 105 110
 Cys Leu Gly Ile Ser Pro Phe Glu Val His Ala Trp Leu Leu Pro Lys
 115 120 125
 Asp Leu Leu Leu Glu Tyr Val Ile Gly His Met Gly Gln His Thr Gly
 130 135 140
 Ala Ser Gly Ser Asp Thr Ala Trp Leu Gly Phe Pro Ala Asp Glu Pro
 145 150 155 160
 Tyr Asp Trp Met Arg Pro Phe Gly Gly Arg Leu Gly His Val Glu Asp
 165 170 175
 Leu Leu Leu Ala Ala Gly Pro Gly Pro Tyr
 180 185

<210> 9
 <211> 413
 <212> DNA
 <213> Escherichia coli

<400> 9
 accggtgatt ggacattgcc gaaatcaggc tgtctctcac tatttgacgc actggctgga 60
 ctatccacat ctaccttatt cccccgaata acgagatccc ttccagcacc gggcaattgc 120
 ccggtttttt ttgcgttgaa tttgtcattt tgtgccgtgg tgtttaaacc gcacagaata 180
 aattgtcgtg atttcacctt taaaataaaa ttaaaagaga aaaaaattct ctgtggaagg 240
 gctatgtag ataaaattga ccgtaagctg ctggccttac tgcagcagga ttgcaccctc 300
 tctttgcagg cactggctga agccgttaat ctgacaacca ccccttgctg gaagcgctg 360
 aaacggctgg aggacgacgg tatccttatc ggcaaagtcg ccctgctgga tcc 413